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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶: A61K 39/12, C12N 7/00, 7/02, C12P 13/04, 13/24, 13/22, 13/20, 13/14, 13/08	A1	(11) International Publication Number: WO 97/31652 (43) International Publication Date: 4 September 1997 (04.09.97)
(21) International Application Number: PCT/US97/03126 (22) International Filing Date: 28 February 1997 (28.02.97) (30) Priority Data: 08/609,334 1 March 1996 (01.03.96) US (71) Applicant: THE UNITED STATES OF AMERICA, represented by THE SECRETARY OF AGRICULTURE [US/US]; Washington, DC 20250-1400 (US). (72) Inventors: WESLEY, Ronald, D.; 4719 Dover Drive, Ames, IA 50014 (US). CLOUSER, Deborah, F.; 2825 Monroe Drive, Ames, IA 50010 (US). MENGELING, William, L.; 4220 Phoenix, Ames, IA 50014 (US). ANDREYEV, Vladimir G.; Apartment 1, 4 Krasnoznamyonnaya Street, Vladimir, Vladimir'S (RU). VORWALD, Ann, C.; 1804 Douglas Avenue, Ames, IA 50010 (US). LAGER, Kelly, M.; R.R. 1, Box 122, Nevada, IA 50201 (US). (74) Agents: PENDORF, Stephan, A. et al.; Suite 1000, 600 N. Westshore Boulevard, Tampa, FL 33609 (US).	(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>	
(54) Title: RESTRICTION ENZYME SCREEN FOR DIFFERENTIATING PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS STRAINS (57) Abstract A test based on restriction enzyme analysis identifies and differentiates strains of porcine reproductive and respiratory syndrome virus (PRRSV). Amplified cDNA from the ORF 5 region of the viral genome has been targeted for identification of unique restriction sites that allow for the differentiation of the vaccine strain from field strains, and for differentiation of field strains from each other through the use of selected restriction enzymes. This assay is useful for both clinical diagnosis of PRRSV field strains in vaccinated pigs as well as for epidemiological studies in the evaluation of the source and transmission of PRRS field viruses.		

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RESTRICTION ENZYME SCREEN FOR DIFFERENTIATING PORCINE
REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS STRAINS

Background of the Invention

Field of the Invention

This invention relates to a differential test for distinguishing strains of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) from one another and for differentiating field strains from the currently used vaccine strain.

Porcine reproductive and respiratory syndrome (PRRS) was first reported in North America in 1987 (Keffaber, 1989) and emerged in Europe in late 1990 (Wensvoort et al., 1991). Recently, PRRS has gained world-wide attention because of its economic impact on the swine industry. The disease is characterized by reproductive failure in pregnant sows and respiratory problems in pigs of all ages (Loula, 1991). The causative agent of PRRS is a small (50-60nm) positive-stranded RNA enveloped virus. The genome is a polyadenylated RNA molecule of about 15 kb and contains eight open reading frames (ORFs). Viral proteins are expressed by six subgenomic mRNAs which are transcribed from the negative strand using a body sequence derived from the 5' end of the viral genome (Meulenberg et al., 1995). The virus replicase is most likely encoded by ORFs 1a/1b by a -1 frameshift (Conzelmann et al., 1993). Open reading frames 2 to 4 encode for putative structural proteins (Van Nieuwstadt, 1995). ORF 5 encodes for a envelope (E) glycoprotein of approximately 25 kDa. A non-glycosylated membrane (M) protein of 18 kDa is encoded by ORF 6 and the nucleocapsid (N) protein of 15 kDa is encoded by ORF 7 (Meulenberg et al., 1995; Conzelmann et al., 1993).

Morphologically and morphogenetically, PRRSV resembles equine arteritis virus (EAV), lactate dehydrogenase-elevating

virus (LDV), and simian hemorrhagic fever virus (SHFV) (Conzelmann et al., 1993; Meulenberg et al., 1993; Plagemann and Moennig, 1991; Snijder and Spaan, 1995). As a result of common features shared by these viruses, they have been tentatively grouped into a new virus family, Arteriviridae (Conzelmann et al., 1993; Meulenberg et al., 1993, Plagemann and Moennig, 1992).

Description of the Prior Art

Although the clinical features of PRRS in the United States and in Europe appear similar, several recent studies have indicated phenotypic, antigenic, and genetic differences exist among PRRSV isolates (Bautista et al., 1993; Meng et al., 1994; Wensvoort et al., 1992). The amino acid sequences of ORF 2 through ORF 7 of North American isolates share only 55-79% homology with those of European descent (Meulenberg et al., 1995). It is believed that the glycosylated structural envelope protein E, encoded by ORF 5, is partially responsible for these serological variations among isolates of PRRSV (Meulenberg et al., 1995). Protein E is the counterpart of G_L of EAV (de Vries et al., 1992) and VP-3 of LDV (Gogeny et al., 1993). Both (G_L and E) proteins contain a large internal hydrophobic region which has been thought to anchor these proteins in the membrane (Meulenberg et al., 1995). The existence of neutralizing epitopes in VP-3 of LDV (Harty and Plagemann, 1988) and G_L of EAV (Balasuriya et al., 1995) was demonstrated using monoclonal antibodies and sequencing escape mutants. More recent studies indicate that protein E plays a role in inducing neutralizing antibodies (Persch et al., 1995).

A modified-live-virus vaccine strain RespPRRS® of PPRSV is currently used in the United States for the prevention of the respiratory facet of the syndrome. Although the vaccine strain

is attenuated, it, like virulent field strains of PRRSV, has the ability to persist for at least several weeks in a vaccinated pig. Consequently, the source of PRRSV isolated from diagnostic samples is sometimes in question and it would be highly desirable to have a positive assay for identifying the source.

Summary of the Invention

We have now discovered that ORF 5 can be targeted in a restriction enzyme analysis for distinguishing vaccine strain RespPRRS® of PRRSV from virulent field strains and also for distinguishing field strains from one another. The reading frame is first converted to a double stranded DNA, amplified, and then cut with restriction enzymes in conserved regions which collectively have sufficient variability among strains to permit generation of a unique fragment profile for each strain of PRRSV.

In accordance with this discovery, it is an object of the invention to provide a tool for distinguishing vaccine strain RespPRRS® from wild-type field strains.

It is also an object of the invention to provide a tool for epidemiological studies in the evaluation of the source and transmission of field strains of PRRSV.

It is also an object of the invention to provide a sensitive, reliable, and rapid assay for PRRSV suitable for large-scale herd screening.

A further object of the invention is to provide a diagnostic basis for designing an effective control program for PRRS in swine herds.

Other objects and advantages of this invention will become readily apparent from the ensuing description.

Brief Description of the Drawing

FIG. 1 shows the aligned ORF 5 sequences for field strain VR 2332 and vaccine strain RespPRRS® of PRRSV as well as the consensus sequence for these strains.

FIG. 2 shows the aligned ORF 5 nucleotide sequences for the 22 field strains and strain RespPRRS® of PRRSV sequenced in conjunction with the invention, and for strain VR 2332 (previously sequenced by others) as compared to the consensus sequence.

FIG. 3 is a computer generated schematic diagram of Mlu I, Sfc I, Hinc II and Sac II ORF 5 cDNA fragments for PRRSV field strain NADC-8 (F) and vaccine strain RespPRRS® (V).

Detailed Description of the Invention

The primary points of novelty regarding the identification and distinction of individual strains of PRRSV in accordance with this invention include: (1) identification of a segment of the viral genome that is sufficiently variable among strains to allow differentiation, yet stable enough so that there is a low probability of mutational changes during repeated in vitro or in vivo passages of a particular strain; (2) selection of a universal set of primers that allows for reverse transcription (RT) and polymerase chain reaction (PCR) amplification of this segment; and (3) identification of unique restriction sites that allow for the differentiation of vaccine strains from field strains, and field strains from one another.

Insofar as currently known, ORF 5 is the only region of the PRRSV genome that has the proper combination of nucleotide variability among strains of PRRSV (exemplified by those listed in Table I) together with long term stability to allow for restriction enzyme differentiation. On the other hand, the stability of the ORF 5 nucleotide sequence of a particular

strain is indicated (FIG. 1) by the fact that there are only two base differences (positions 38 and 451) between vaccine strain RespPRRS® (indicated in the figure as "resp.PRRS"), which was attenuated by repeated serial passages in cell culture, and its presumed parental strain VR 2332. These two strains (which could be considered variations of the same strain) are indistinguishable on the basis of restriction patterns associated with any of the 77 restriction enzymes reported in Table II.

FIG. 2 clearly depicts variations in the ORF 5 nucleotide sequences for strain RespPRRS® of PRRSV sequenced in conjunction with the invention and for 23 field strains of PRRSV, including 22 field strains sequenced in conjunction with the invention and VR 2332 (the sequence of which was previously reported in the literature). The consensus sequence for the 24 strains is also given in the figure. The position and frequency of these variations are sufficient to permit differentiation of every field strain (except presumed parental strain VR 2332) from the vaccine strain using a singular enzyme, either *Mlu* I or *Sfc* I (see Tables I and II). Assaying with both enzymes provides confirmation. As best shown in Table I, a high degree of assurance can be obtained by comparing the combined fragment patterns from *Mlu* I, *Sfc* I, *Hinc* II, and *Sac* II. All 23 of the field strains in Table I can be differentiated from one another by means of an appropriate combination of six or fewer restriction enzymes selected by reference to Table II. In Table II, the PRRSV strains are shown across the top and 77 enzymes which were evaluated for purposes of the invention are indicated on the left. The last column represents the cut sites for both strain RespPRRS® and its presumed parental strain VR 2332. Even though there are two base differences between the ORF 5 of these two strains, the cutting sites in the respective ORF 5 cDNAs are

the same for all of the 77 enzymes shown in the table. The numbers shown in the table cells represent the size of the resultant fragments obtained by cutting a 716 bp amplified DNA including the ORF 5. Multiple fragment sizes are listed in order from 5' to 3'. The symbol "xxx" indicates that the particular enzyme does not cleave anywhere within the 716 bp fragment.

Given that the PRRSV genome is RNA, the region coding for ORF 5 must first be reverse transcribed by methods known in the art to produce double stranded cDNA. By means of PCR or any other like process, the coding region is then amplified to the extent necessary for the subsequent restriction enzyme analysis.

Primers are preferably selected from nearby flanking regions upstream and downstream from the reading frame.

Example 1

Cell and Virus Propagation.

MARC-145 cells (Kim et al., 1993, herein incorporated by reference) were cultured in Eagle's minimum essential medium (MEM), supplemented with 5% fetal bovine serum (FBS) and antibiotics. Twenty-two field strains of PRRSV isolated from Canada, Guatemala, and the United States as well as vaccine strain RespPRRS® of PRRSV were propagated and then cloned by three rounds of end point dilutions on MARC-145.

RNA extraction and Reverse Transcriptase Polymerase Chain Reaction.

Viral RNA was isolated from 22 field strains and vaccine strain RespPRRS® of PRRSV (see Table I) using a standard guanidinium isothiocyanate method (Sambrook et al., 1989, herein incorporated by reference). Single tube reverse transcriptase polymerase chain reactions (RT-PCR) as described by Sellner et

al. (1992, herein incorporated by reference) with slight modifications were conducted on RNA isolated from each of the 23 strains in a Perkin-Elmer 4800[®]. Primers were designed based on the nucleotide sequence of field strain VR 2385 (Meng et al., 1995; Morozov et al., 1995, both herein incorporated by reference) and synthesized by Integrated DNA Technologies, Inc. (Coralville, IA). The sense primer was 5'-CCATTCTGTTGGCAATTTGA-3' (SEQ ID NO:25) and the anti-sense primer was 5'-GGCATATATCATCACTGGCG-3' (SEQ ID NO:26). In SEQ ID NO:27 (which is similar to SEQ ID NO:23 for ORF 5 of vaccine virus RespPRRS but additionally shows the immediate flanking regions), the sense primer extends from nucleotide 1 through nucleotide 20 and the antisense primer is the complement to the nucleotide sequence extending from nucleotide 716 to 697. A 716 bp piece encompassing ORF 5, with flanking regions of ORF 4 and ORF 6, was generated for all strains and the fragments were purified using a GENECLAN[®] kit (Bio 101).

Sequencing.

Double stranded nucleotide sequencing (Tabor and Richardson, 1987, herein incorporated by reference) with Taq polymerase and fluorescently labelled dideoxynucleotides (Applied Biosystems International, Prism System) as described in Sanger et al. (1977, herein incorporated by reference) was performed in triplicate on both strands for analysis with an Applied Biosystems 373A[®] automated sequencer. The same primer set as described above was used for sequencing. Nucleotide sequence editing and alignments were performed using Intelligenetics, GENWORKS[®] version 2.2 software.

Analysis.

To determine the rate of possible drift of ORF 5 sequence, four PRRSV strains of U.S. origin: NADC-8, NADC-9, 41572-2, and 18310-A were repeatedly passed on MARC-145 cells. NADC-8, NADC-9, and 41572-2 encountered 61 passages, and 18310 encountered 31 passages. RT-PCR was performed and the subsequent product was sequenced as described above.

Sequencing of the four selected strains passed in vitro revealed: 6 nucleotide and 4 amino acid substitutions (2,110,136,194 a.a.) for NADC-8; 2 nucleotide and 1 amino acid substitution (59 a.a.) for NADC-9; 2 nucleotide and 2 amino acid substitutions (3, 34 a.a.) for strain 41572-2; and 4 nucleotide and 2 amino acid substitutions (3,194 a.a.) for strain 18310-A (data not shown). However, none of these changes affected restriction patterns of any of these four strains.

Comparison of Sequences.

The complete ORF 5 gene sequence for each of 22 PRRSV field strains and for the vaccine strain RespPRRS[®] was determined. The sequences for the field strains are shown in the SEQUENCE LISTING as SEQ ID NOS:1-22, that for field strain VR 2332 (previously published) is shown as SEQ ID NO:23, and that for vaccine strain RespPRRS[®] is shown as SEQ ID NO:24. These sequences were aligned and compared (FIG. 2) to the consensus sequence for all 24 strains. Alignment analysis indicates the same initiation and termination sites exist for all 24 strains.

Regions of high and low variability are also apparent. Insertions and deletions were found to be nonexistent on the nucleotide level.

Example 2

To differentiate the vaccine strain RespPRRS[®] and the presumed parental field strain VR 2332 from the 22 remaining (field) strains shown in Table I, it was necessary to select one or more appropriate restriction enzymes. The selection was based on a comparison of the ORF 5 sequence data for these strains in conjunction with the known cut sites for the enzymes as summarized in Table II. Using this technique, enzymes *Mlu* I, *Sfc* I, *Hinc* II and *Sac* II were initially selected. The enzymes *Mlu* I and *Sfc* I cut only the vaccine strain RespPRRS[®] and field strain VR 2332, and do not cut any of the other 22 PRRSV strains shown in Tables I and II. The restriction enzymes *Hinc* II and *Sac* II cut most of the PRRSV strains tested giving various gel patterns. Only strains 4 and 9 have a *Hinc* II gel pattern identical to the RespPRRS[®]/VR 2332 gel pattern. A second gel analysis with *Sac* II differentiates the vaccine strain and VR 2332 from PRRSV field strains 4 and 9. The combined results with the 4 restriction enzymes give a high degree of assurance of the RespPRRS[®]/VR 2332 genotype.

Restriction enzymes *Mlu* I and *Sfc* I are particularly valuable for differentiation because these enzymes cut only strain RespPRRS[®]/VR 2332 and none of the other 22 strains of PRRSV. *Mlu* I recognizes the 6 base pair sequence A'CGCGT. For the other 22 PRRSV strains, there are two base differences, namely, guanines at positions 409 and 411; both need to occur in order to create a functional *Mlu* I site. Since two bases need to change for the other strains of PRRSV, the *Mlu* I pattern is a strong marker for the RespPRRS[®]/VR 2332 genotype. Also *Sfc* I only cuts the RespPRRS[®]/VR 2332 PCR-amplified DNA fragment. However, 9 of the 22 other strains of PRRSV require only a single nucleotide change, in the localized 6-nucleotide cutting site, to create a functional *Sfc* I site. Therefore, mutations

resulting in *Sfc* I cutting are potentially more frequent than those for *Mlu* I cutting. As a safeguard against erroneous identification resulting from such mutations, it is advisable to conduct the assay with additional enzymes.

A typical gel electrophoresis test, in which vaccine strain RespPRRS® and strain NADC 8 are compared after digestion with *Mlu* I, *Sfc* I, *Hinc* II and *Sac* II, is represented by FIG. 3. The *Mlu* I and *Sfc* I gel patterns of strain NADC 8 are the same for all 22 PRRSV strains and distinct from strain RespPRRS®/VR 2332 gel pattern. For restriction enzymes *Hinc* II and *Sac* II, strain NADC-8 gel patterns are also distinct from strain RespPRRS®/VR 2332 patterns, but similar to other PRRSV strains. However, all of the PRRSV strains in Table II can be differentiated one from another by appropriate selection of restriction enzymes. No more than 6 restriction enzymes would be needed for differentiating the strains reported in Table II.

Example 3

The constancy of the restriction enzyme pattern within ORF 5 during persistent infection of pigs with PRRSV was evaluated for the purpose of assessing the validity of the assay described in Example 2. Virus stability upon PRRSV replication *in vivo* was studied in four individual gilts, in penmates, and in gilt-piglet relationships. The results are shown in Table III, below. In each of evaluations Nos. 1-3, the virus was passaged *in vivo* in a gilt for a period of 7 weeks. After this time, virus was isolated from a sample taken by lung lavage wherein the alveolar macrophages, which are believed to be the primary cells for virus replication *in vivo*, are flushed from the lung.

In each case, the recovered strain was characterized by the same RE pattern as the exposure strain (RespPRRS®). In evaluation No. 4, the same results were obtained for strain

NADC-8. In evaluation Nos. 5 and 6, a pig was exposed to strain NADC-8, and 8 weeks later brought into contact with a second pig which thereafter shared the same pen. After 3 weeks, the RE pattern of the strain recovered from the second pig was identical to that of Strain NADC-8 used to infect the first pig.

In evaluation No. 7, a pregnant gilt was infected with strain RespPRRS® eight weeks prior to farrowing. The RE pattern of the PPRSV recovered 5 weeks later from one of her piglets was the same as the original strain RespPRRS®.

It is understood that the foregoing detailed description is given merely by way of illustration and that modifications and variations may be made therein without departing from the spirit and scope of the invention.

TABLE I

Restriction Enzyme Analysis of PRRSV Isolates

Strains	ID	Origin	Year	Restricted Enzyme ^a			
				<i>Mlu</i> I	<i>Sfc</i> I	<i>Hinc</i> II	<i>Sac</i> II
1	46448	IA	1989	-	-	219	24
2	46907	KY	1991	-	-	-	24
3	1205-D	MO	1992	-	-	-	24
4	10654	IA	1992	-	-	360	-
5	30093-A	IL	1992	-	-	219	24
6	34075	NE	1992	-	-	88,219	24
7	49138	TX	1992	-	-	88,219	24
8	5556	MI	1993	-	-	-	24,555
9	22805	KS	1992	-	-	260	555
10	5591	NC	1993	-	-	219	24
11	14622	AR	1993	-	-	88	24,555
12	19950-E	MN	1993	-	-	88,219	24
13	26948-2	VA	1993	-	-	88	24,555
14	41572-2	NE	1993	-	-	88,219	24,555
15	42928	IL	1993	-	-	88,219	24
16	32983-LG	NC	1993	-	-	88,219	24
17	30352-3	MI	1993	-	-	-	24,555
18	47324-2	CANADA	1993	-	-	88	24,555
19	18310-A	PA	1994	-	-	88	24
20	24901	GUATEMALA	1994	-	-	88,219	24
NADC-8	(IA)-92	IA	1992	-	-	219	24,555
NADC-9	(IA)-93	IA	1993	-	-	219	24,555
RespPRRS®	-	MN ^b		408	116	360	24
VR 2332	-	MN		408	116	360	24

^a The designated cut sides are for the 603 bp ORF 5^b Presumed to originate from strain VR 2332

Table II (A)

ENZYME	#1	#2	#3	#4	#5	#6	#7	#8	#9	#10	#11	#12
Acc I	318	318	318	318	318	xxx	xxx	318	318	318	318	318
Aha II	xxx	268	268	118	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Aku I	multi(4)	multi(4)	multi(4)	multi(4)	multi(5)	136/176	136/176	136/176/198	multi(4)	136/176	136/176	136/176
Apr II	xxx	xxx	xxx	xxx	xxx	268	268	xxx	xxx	268	xxx	268
Bal I	140/204	xxx	204	xxx	140/204	204	204	204	xxx	204	204	204
Bcl I	xxx	309	309	xxx	xxx	555	xxx	309	xxx	xxx	309	xxx
Bcl II	267	267	267	267	267	xxx	xxx	267	267	xxx	xxx	xxx
Bbv I	145/368	145/368	145/368	145/368	145/368	145/368	145/368	142/145/368	145/368	145	145/368	multi(5)
Bla I	195/280	195/280	195	195/445	195/280/378	308/465/629	465/629	195/198/378	195/445	929	xxx	280/465/629
Bla II	xxx	268	268	118	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Bsa I	493/76580	493/76580	493/76580	493/76580	49580	multi(4)	49580	493/76580	493/76580	49580	493/76580	493/76580
Bst EI	498	498	498	498	498	498	498	xxx	498	498	498	498
Bst II	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Bst III	263	263	263	263	263	xxx	xxx	xxx	263	xxx	263	xxx
Bst IV	272/377	377	377	112/272/377	272/377	112/272/377	112/272/377	272/377	112/272/377	112/272/377	112/272/377	112/272/377
Bst V	xxx	324	324	xxx	xxx	324	xxx	xxx	xxx	xxx	xxx	xxx
Bst VI	216	xxx	xxx	xxx	216	xxx	195	xxx	xxx	xxx	xxx	xxx
Bst VII	xxx	xxx	xxx	xxx	xxx	540	xxx	498	xxx	xxx	xxx	540
Bst VIII	378/428	378/428	378/428	378/428	308/428	378/428	428	378	378/428	428	378/428	378/428
Bst IX	51/268	multi(4)	51/65/268	65/268	51/268	51/268	51/65/268	multi(4)	65/268	multi(4)	multi(4)	51/65/268
Cir I	xxx	324	324	xxx	xxx	324	xxx	xxx	xxx	xxx	xxx	xxx
Cla I	xxx	xxx	xxx	550	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Dde I	351/472/628	351/472/628	351/472/628	351/472/628	351/472/628	xxx	472	351/472	351/472/628	472	351/472/628	199/472
Dpn I	549	549	549	549/553	549	xxx	549	549	553	497/549	549	549
Dpn II	547	xxx	547	547/551	547	xxx	547	547	551	495/547	547	547
Eae I	xxx	307	307	xxx	xxx	583	xxx	307	xxx	379	307	xxx
Eae II	510	xxx	xxx	610	510	xxx	xxx	xxx	510	xxx	xxx	xxx
Eco 47III	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Eco 2I	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Fnu 4HI	134/382	134/382	134/382	134/382	134/382	134/382	134/382	multi(4)	134/382/583	134/382	134/382/583	multi(5)
Fok I	xxx	xxx	xxx	xxx	xxx	xxx	xxx	610	xxx	xxx	610	xxx
Hae II	121/434	121/271/434	121/271/434	434	121/434	434	434	121/434	434	434	434	434
Hae III	xxx	309	309	xxx	304	555	541	309	xxx	381/541	309	xxx
Hpa I	173	173	173	128/173	173	173	173	173	173	173	173	173
Hol AI	xxx	xxx	xxx	112	xxx	112/272	112/272/377	xxx	112	112/272/377	112	112/272
Hha I	110/120/433	multi(4)	multi(4)	433	110/120/433	433	433	110/120/433	433	433	379/433	433
Hinc II	247	xxx	xxx	388	247	118/247	118/247	xxx	388	247	118	118/247
Hinf I	248/481	248/481	248/481	248/481	248/481	248/481	248/481	248/481	248/481	248/481	248/481	248/481

Table II (B)

ENZYME	813	814	815	816	817	818	819	820	NAOC-8	NAOC-9	REF. NZ332
Acc I	318	xxx	xxx	318	318	xxx	xxx	xxx	xxx	xxx	318
Aha II	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Alu I	138/178	138/178	138/178	138/178	138/178	138/178	138/178	138/178	multi(4)	multi(4)	multi(4)
Apo II	268	268	268	268	268	268	268	268	xxx	xxx	xxx
Apo I	204	204	204	204	204	204	204	204	1402/04/601	1402/04/601	204
Bal I	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Ban I	xxx	xxx	xxx	xxx	267	267	xxx	xxx	267	267	267
Bbv I	multi(4)	multi(4)	145/268	multi(7)	145/268	145/268	145/268	multi(4)	145/268	145/268	145/268
Bfi I	465/678	280/678	678	280/465/678	xxx	280	972	972	195/280	195/280	195
Bsa HI	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Bsa II	493/76/580	multi(4)	493/76/580	493/76/580	493/580	multi(4)	493/580	493/580	493/76/580	493/76/580	493/76/580
Bcl I	498	498	498	498	xxx	498	498	xxx	498	498	498
Bcl I	xxx	xxx	xxx	xxx	xxx	xxx	325	325	xxx	xxx	xxx
Bem AI	xxx	xxx	216	xxx	263	xxx	216/630	216	263	263	263
Bsp I	112/272/377	112/272/377	112/272/377	112/272/377	272/377	112/272	112/272/377	112/272/377	272/377	272/377	112/272/377
Bst FI	xxx	324	324	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Bst I	xxx	xxx	xxx	xxx	xxx	xxx	195	xxx	218	218	xxx
Bst EB	308	540	xxx	xxx	498	xxx	540	540	540	540	xxx
Bst MI	378/478	378/478	983/78/478	378/478	478	378/478	478	478	378/478	378/478	378/478
Bst NI	multi(4)	multi(4)	516/5/566	516/5/566	multi(4)	multi(4)	516/5	516/5/566	51/268/582	51/268/582	multi(4)
Cfr I	xxx	324	324	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Cla I	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Cla I	351/472	xxx	472	472	351/472/828	351/828	472	472	351/472/828	351/472/828	351/472/828
Dpn I	549	549	497/549	549	549	xxx	549	549	549	549	549
Dpn II	547	547	495/547	547	547	xxx	547	547	547	547	547
Eae I	xxx	xxx	xxx	xxx	307	xxx	xxx	xxx	xxx	xxx	xxx
Eat I	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Eco 47III	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Epp II	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Ery 4HI	multi(5)	multi(5)	134/382	multi(7)	134/382/583	134/382/583	134/382	multi(4)	134/382/583	134/382/583	134/382
Fok I	xxx	xxx	xxx	xxx	610	xxx	xxx	xxx	xxx	xxx	xxx
Hae II	434	434	130/434	434	121/434	434	434	434	121/434	121/434	434
Hae II	xxx	xxx	541	xxx	309	xxx	xxx	55	xxx	xxx	xxx
Hga I	173	173	173	173	173	173	173	173	173	173	173
Hha I	112/272	112/272	112/272	112/272	xxx	112	112/272/377	112/272/377	xxx	xxx	112
Hho I	433	433	128/433	433	110/120/433	375/433	433	433	110/120/433	110/120/433	433
Hinf II	116	116	116	116	116	116	116	116	247	247	388
Hind I	481	248/481	248/481	248/481	248/481	248/481	248/481	248/481	248/481	248/481	248/481

Table II (C)

ENZYME	#1	#2	#3	#4	#5	#6	#7	#8	#9	#10	#11	#12
Alind P1	108/118/431	mmH(4)	mmH(4)	431	108/118/431	431	431	108/118/431	431	431	373/431	431
Alpa II	325	325	325	325	325	325	325	325	325	325	325	325
Alph I	xxx	xxx	xxx	268	xxx	268/534	268	47/490	xxx	268	xxx	534
Alsi I	xxx	267	267	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Alsi I	195/280	195/199	195	195/445	195/280/378	306/465/629	465/629	195/199/628	195/445	629	xxx	280/465/629
Alsi II	308	593	593	308	308	308/540	308	495	308	308/333	593	308/540
Alsi I	547	547	547	547/551	547	xxx	547	547	551	495/547	547	547
Alsi II	425/453/527	324/425/453	324/425/453	425/453/527	425/453/527	324/425/453	425	227/453	425/527	425	425/453	425
Alsi I	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Alsi I	mmH(4)	289/523/584	289/523/584	289/523/584	mmH(4)	523/584	471/523/584	289/523/584	289/510/523	523/584	289/523/584	523/584
Alsi I	xxx	309	309	xxx	xxx	585	xxx	309	xxx	xxx	309	xxx
Alsi I	xxx	xxx	xxx	xxx	xxx	594	594	xxx	xxx	594	xxx	387/594
Alsi I	325	325	325	325	325	325	325	325	325	325	325	325
Alsi I	66	xxx	xxx	147/288	66	xxx	xxx	xxx	147/288	xxx	xxx	xxx
Alsi I	xxx	269	269	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Alsi I	326	xxx	xxx	326	326	xxx	326	326	326	326	xxx	326
Alsi I	194	184	194	194	194	xxx	xxx	194	194	xxx	xxx	xxx
Alsi I	425/442	425/442	425/442	425/442	425/442	425/442	425/442	425/430/442	425/442	425/442	425	425
Alsi I	269/578	269/578	269/578	269/578	269/578	578	578	269/578	269/578	578	578	578
Alsi I	xxx	65	65	65	xxx	xxx	65	65	65	65	65	65
Alsi I	51/149	51/149/609	51/149/609	609	51/149	51/609	51	51/582/609	582/609	51/609	51/582/609	51/609
Alsi I	425	425	425	425	425	425	425	425	425	425	425	425
Alsi I	242/475	242/475	242/475	242/475	242/475	242/475	242/475	242/475	242/475	242/475	242/475	242/475
Alsi I	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Alsi I	149	149	149	xxx	149	xxx	xxx	xxx	xxx	498	xxx	xxx
Alsi I	443	443	443	443	443	443	443	443	443	443	443	443
Alsi I	52	52	52	xxx	52	52	52	52/583	583	52	52/583	52
Alsi I	547	547	547	547/551	547	xxx	547	547	551	495/547	547	547
Alsi I	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Alsi I	378/428	378/428	378/428	378/428	306/328/428	378/428	378/428	378/428	378/428	378/428	378/428	378/428
Alsi I	493/765/80	493/765/80	493/765/80	493/765/80	493/765/80	mmH(4)	493/765/80	493/765/80	493/765/80	493/765/80	493/765/80	493/765/80
Alsi I	367	367	367	367	367	367	367	302/367	367	367	367	367
Alsi I	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Alsi I	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Alsi I	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Alsi I	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Alsi I	535/550	535/550	535/550	550	535/550	550	535/550	535/550	535	535/550	535/550	535/550
Alsi I	297	297	xxx	xxx	297	297	297	297	297	297	297	297
Alsi I	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx
Alsi I	461	461	461	461	xxx	xxx	xxx	461	461	461	461	xxx

Table II (D)

[illegible]

TABLE III

Restriction Enzyme Pattern after PRRSV Replication in vivo

Sample		Duration of		PRRSV Strain	
No.	Type	Source	Infection	Exposure	Recovered
1	Lung-Lavage	Gilt	7 wks	RespPRRS®	RespPRRS®
2	"	"	"	"	"
3	"	"	"	"	"
4	"	"	"	NADC-8	NADC-8
5	"	Pig-Pig	8 + 3	"	"
6	"	"	8 + 3	"	"
7	"	Gilt-Piglet	8 + 5	RespPRRS®	RespPRRS®

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: The United States of America, as
Represented by the Secretary of
Agriculture
- (ii) TITLE OF INVENTION: Restriction Enzyme Screen for
Differentiating Porcine Reproductive and Respiratory
Syndrome Virus Strains
- (iii) NUMBER OF SEQUENCES: 27
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Curtis P. Ribando
 - (B) STREET: 1815 N. University Street
 - (C) CITY: Peoria
 - (D) STATE: IL
 - (E) COUNTRY: USA
 - (F) ZIP: 61604
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Ribando, Curtis P.
 - (B) REGISTRATION NUMBER: 27,976
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 309-681-6513
 - (B) TELEFAX: 309-681-6688

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 46448 (IA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGTTGGGTA AATGCTTGAC CGCGGGCTGT TGCTCGCAAT TGCTTTTTTG GTGGTGTATC	60
GTGCCGTCTT GTTTTGTTC GCTCGTCAGC GCCAACGGGA ACAGCAGCTC AAATTTACAG	120
CTGATTTACA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TAATAAATTT	180
GACTGGGCAG TGGAGTGTTT TGTCATTTTT CCCGTGTTGA CTCACATTGT CTCTTATGGT	240
GCCCTCACTA CTAGCCATTT CCTTGACACA GTCGGTCTGG TCACTGTGTC TACCGCCGGG	300
TTTGTTACAG GCGGGTATGT TCTGAGTAGC ATCTACGCGG TCTGTGCCCT GGCTGCGTTG	360
ATTTGCTTCG TCATTAGGTT TGC GAAGAAT TGCATGTCCT GCGCTACTC ATGTACCAGA	420
TATACCAACT TTCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCCTGTCATC	480
ATAGAGAAGA GGGGTAAAGT TGAGGTCGAA GGTCACTGA TCGACCTCAA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTATAACC AAAGTTTCAG CAGAACAATG GGGTCGTCCT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory
Syndrome Virus
- (B) STRAIN: 46907(KY)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTTTTTT GTGGTGTATC	60
GTGCCGTCCT GTTTTGTTC GCTCGTCAGC GCCAACAGCA ACAGCAGCTC CCATTTACAG	120
CTGATTTACA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TAGTAGATTT	180
GATTGGGCAG TGGAGTGTTC TGTCATCTTT CCTGTGCTGA CTCACATTGT CTCCTATGGC	240
GCCCTCACTA CCAGCCATTT CCTTGACACA GTCGGTCTGG CCACTGTGTC TACCGCCGGT	300
TTTCTTCGCG GCGGTATGT TCTGAGTAGC ATCTACGCGG TCTGTGCCCT GGCTGCGTTG	360
TTTGTCTTCG TCATTAGATT GCGAAGAAT TGCATGTCCT GCGCTATTTC ATGTACCAGA	420
TATACCAACT TTCTTCTGGA TACTAAGGGC AGACTCTATC GTTGGCGGTC GCCCGTCATC	480
ATAGAGAAAA AGGGTAAAGT TGAGGTCGAA GGTCACTGA TCGACCTCAA GAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTGTAACC AGAGTTTCAG CGGAACAATG GGGTCGTCCT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory
Syndrome Virus
- (B) STRAIN: 1205-D(MO)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTTTTTT GTGGTGTATC	60
GTGCCGTCCT GTTTTGTGTC GCTCGTCAGC GCCAACAGCA ACAGCAGCTC TCATTACAG	120
CTGATTTACA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TAATAAATTT	180
GATTGGGCAG TGAATGTTT TGTCACTTTT CCTGTGCTGA CTCACATTGT CTCCTATGGC	240
GCCCTCACTA CCAGCCATTT CCTTGACACA TTCGGTCTGG CCACTGTGTC TACCGCCGGT	300
TTTCTTCACG GCGGTATGT TCTGAGTAGC ATCTACGCGG TCTGTGCCCT GGCTGCGTTG	360
TTTGCTTCG TCATTAGATT TGCGAAGAAT TGCATGTCCT GCGCTATTTC ATGTACCAGA	420
TATACCAACT TTCTTCTGGA TACTAAGGGC AGACTCTATC GTTGGCGGTC GCCCGTCATC	480
ATAGAGAAAA AGGGTAAAGT TGAGGTCCAA GGTCACTGA TCGACCTCAA GAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTGTAACC AGAGTTTCAG CGGAACAATG GGGTCGTCCT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 10654 (IA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCAAT TGCTTTTTTT GTGGTGTATC	60
GTGCCGTCTT GTCTTGTTGC GCTCGTCAGC GCCAACGGGA ACAGCAGCTC AAATTTACAG	120
CTGATTTACA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TAATAAATTT	180
GACTGGGCAG TGGAGTGTTT TGTCATTTTT CCCGTGTTGA CTCACATTGT CTCTTACGGT	240
GCCCTCACTA CTAGCCATTT CCTTGACACA GTCGGCCTGG TCACTGTGTC TACCGCCGGG	300
TTTGTTACAG GCGGTATGT TCTGAGTAGC ATCTACGCGG TCTGTGCCCT AGCTGCGTTG	360
ATTTGCTTCG TCATTAGGTT TGCGAAGAAT TGCATGTCCT GCGGCTACTC ATGTACCAGA	420
TATACTAACT TTCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCCCGTCATC	480
ATAGAGAAGA GGGGTAAAGT TGAGGTCGAA GGTCATCTGA TCGACCTCCA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTATAACC AGAGTTTCAG CAGAACAATG GGGTCGTCCT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 30093-A(IL)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCAAT TGCTTTTTTT GTGGTGTATC	60
GTGCCGTCTT GTCTTGTTGC GCTCGTCAGC GCCAACGGGA ACAGCAGCTC AAATTTACAG	120
CTGATTTACA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TAATAAATTT	180
GACTGGGCAG TGGAGTGTTT TGTCATTTTT CCCGTGTTGA CTCACATTGT CTCTTACGGT	240
GCCCTCACTA CTAGCCATTT CCTTGACACA GTCGGCCTGG TCACTGTGTC TACCGCCGGG	300
TTTGTTTCAG GGCGGTATGT TCTGAGTAGC ATCTACGCGG TCTGTGCCCT AGCTGCGTTG	360
ATTTGCTTCG TCATTAGGTT TGCGAAGAAT TGCATGTCCT GGCGCTACTC ATGTACCAGA	420
TATACTAACT TTCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCCCGTCATC	480
ATAGAGAAGA GGGGTAAAGT TGAGGTCGAA GGTCACTCTGA TCGACCTCCA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTATAACC AGAGTTTCAG CAGAACAATG GGGTCGTCCT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 34075 (NE)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTTGCGAT TGCTTTCITT GTGGTGTATC	60
GTGCCGTTCT TTTTGTCTGT GCTCGTCAAC GCCAACAGCA CCAGCAGCTC CCATTGCGAG	120
TTGATTTATA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTGGC TAATAAATTT	180
GATTGGGCAG TGGAGAGTTT TGTTATTTTT CCCGTGTTGA CTCACATTGT TTCCTATGGT	240
GCACTCACCA CCAGCCATTT CCTTGACACA GTCGGTCTAG TTAGTGTGTC CACCGCCGGT	300
TTTCTTCACG GGCGGTATGT CTTGAGTAGC ATCTACGCGG TCTGTGCCCT GGCTGCGTTG	360
GTTTGCTTCG GCATTAGGTT TGCGAAGAAC TGCATGTCCT GCGGCTACTC ATGTACCAGA	420
TATACCAACT TTCTTCTAGA CACCAAGGGC AGACTCTATC GTTGGCGGTC GCCTGTCATC	480
ATAGAGAAAA GGGGTAAGGT TGAGGTCGCA GGTACCTAA TCGACCTCCA AAGAGTTGTG	540
CCTGATGGTT CCGTGGCCAC TCCTTTAACC AGAGTTTCAG CGGAACAATG GGGTCGTCCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 49138 (TX)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTTCTTT GTGGTGTATC	60
GTGCCGTTCT GTTTTGCTGT GCTCGTCAAC GCCAACAGCA ACAGCAGCTC TCATTTTCAG	120
TTGATTTATA ACTTGACGCT ATGTGAGCTG AATGGCACAG ACTGGCTGGC TAACAAATTT	180
GATTGGGCAG TGGAGACTTT TGTCATCTTT CCCGTGTTGA CTCACATTGT TTCCTATGGT	240
GCACTCACCA CCAGCCATTT CCTTGACACA GTTGGTCTGG TTAGTGTC CACCGCCGGG	300
TTTTATCAG GCGGTATGT CTTGAGTAGC ATCTACGCGG TCTGTGCTCT GGCTGCGTTG	360
ATTTGCTTCG TCATTAGGTT TGCGAAGAAC TGCATGTCCT GCGCTACTC ATGTACCAGA	420
TATACCAACT TCCTCCTAGA TACTAAGGGC AGACTCTATC GTTGGCGGTC GCCTGTTATC	480
ATAGAGAAAG GGGGTAAGGT TGAGGTCGAA GGCCACCTGA TCGACCTCCA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC TCCTTTAACC AGAGTTTCAG CAGAACAATG GGGTCGTCCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory
Syndrome Virus
- (B) STRAIN: 5556 (MI)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGTTGGTGA GATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTTTTTT GTGGTGTATC	60
GTGCCGTCCT GTTTTGTTGC GCTCGTCAGC GCCAACATAA GCAGCAGCTC TCATTACAG	120
TTGATTTACA ACCTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TAGTAAATTT	180
GATTGGGCAG TGGAGTGCTT TGTCATCTTC CCTGTGCTGA CTCACATTGT CTCCTATGGT	240
GCCCTCACTA CCAGCCATTT TCTTGACACA GTCGGTCTGG CCACTGTGTC TACCGCCGGG	300
TTTGTTACAG GCGGTATGT TCTGAGTAGC ATCTACGCGG TCTGTGCCCT GGCTGCGTTG	360
ATTTGCTTCG TCATCAGGTT TGTGAAAAAT TGCATGTCAT GCGGCTACTC ATGTACCAGA	420
TATACCAACT TTCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGGTC ACCTGTCATC	480
ATAGAGAAAA AGGTTAAAGT TGAGGTCGAA GGTCACTGA TCGACCTCAA GAGAGTTGTG	540
CTTGATGGTT CCGCGGCAAC CCCTATAACC AGAGTTTCAG CGGAACAATG GGGTCATCCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 22805(KS)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGTTGGGGA AATGCTTGAC CGTGGGCTGT TGCTCGCGAT TGCCTTCCTT GTGGTGTATC	60
GTGCCGTTCT GTTTTGCTGT GCTCGCCAAC GCTCACGGCA ACAGCAGCTC TCATCTGCAA	120
TTGATTTACA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TGATAGATT	180
GATTGGGCAG TGGAGAGCTT TGTCATCTTT CCTGTTTTGA CTCACATTGT CTCCTATGGT	240
GCCCTCACTA CCAGCCATTT CCTTGACACA ATTGCTTTAG TCACTGTGTC TACCGCCGGG	300
TTTGTTTACA GCGGTATGT CCTGAGTAGC ATCTACGCAG TCTGTGCCCT GGCTGCGTTG	360
ACTTGCTTCG TCATTAGGTT TGTAAGAAT TGCATGTCCT GCGCTACTC ATGTACTAGA	420
TATACCAACT TTCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCCTGTCATC	480
ATAGAGAAGA GGGGCAAGGT TGAGGTCGAA GGTCACTGA TTGATCTCAA AAGAGTTGTG	540
CTTGATGGTT CCGCGGCAAC CCCTATAACC AGAGTTTCAG CGGAACAATG GGGTCGTCCT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 5591 (NC)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGTTGGGGA AATGCTTGAC CGCGGATTGT TGCTCGCGAT TGCTTTTTTT GTGGTGTATC	60
GTGCCGTTCT GGTTCGCTGT GCTCGGCAAC GCCAACAGCA CCAGCAGCTC TCACTTACAG	120
TTGATTTATA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGTTGGC TAACAAATTT	180
GATTGGGCAG TGGAGAGTTT TGTATTTTTT CCGTGTGA CTCACATTGT TTCCTATGGT	240
GCACTCACCA CCAGCCATTT CTTGACACA GTCGGTCTGG TTAGTGCTC TACCGCCGGG	300
TTTTGTCACG GGCGGTATGT CTTGAGTAGC ATCTACGCGG TCTGTGCTCT GGCCGCGTTG	360
ATTTGTTTCG TCATCAGGTT TGCGAAGAAC TGCATGTCCT GCGCTACTC ATGTACCAGA	420
TATACCAACT TCCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGATC GCCTGTCATC	480
ATAGAGAAAG GGGTAAGGT TGAGGTCGAA GGCCATCTGA TCGACCTCCA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTTTAACC AGAGTTTCAG CGGAACAATG GGGTCGTCCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 14622 (AR)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCITTCTTT GTGGTTTATC	60
GTGCCGTTCT GTTTTGCTGT GCTCGTCAAC GCCAACAGCA ACAGCAGCTC TCATTACAG	120
TTGATTTATA ACCTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTGGC TAATAAATTT	180
GATTGGGCAG TGGAGAGTTT TGTCACTTTT CCTGTGCTGA CTCACATTGT CTCTTATAGT	240
GCCCTCACTA CCAGCCATTT CCTTGACACA GTCGGTCTGG CCACTGTGTC TACCGCCGGA	300
TTTGTTACAG GCGGGTATGT TCTGAGTAGC ATCTACGCGG TCTGCGCCCT GGCTGCGTTG	360
ATTTGCTTCA TCATCAGGTT TGCGAAGAAT TGCATGTCCT GCGGCTACTC TTGTACCAGA	420
TATACCAACT TTCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCCCGTCATC	480
ATAGAGAAAA GGGGCAAAGT TGAGGTCGAA GGTCACTCTGA TCGACCTCAA GAGAGTTGTG	540
CTTGATGGTT CCGCGGCAAC CCCTGTAACC AAAGTTTCAG CGGAACAATG GGGTCATCCT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 19950-E(MN)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTTCITT GTGGTGTATC	60
GTGCCGTTCT GTTTTGCTGT GCTCGTCAAC GCCAACAGCA GCAGCAGCTC TCATTTTCAG	120
TTGATTTATA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTGGC TGAGAAATTT	180
GATTGGGCGG TGGAAAGTTT TGTCATTTTT CCCGTGTTGA CTCACATTGT TTCCTATGGT	240
GCACTCACTA CTAGCCATTT TCTTGACACA GTCGGTCTGG TTAGTGTC TACCGCCGGG	300
TTTTGGCAGG GCGGTATGT CTTGAGCAGC ATCTACGCGG TCTGTGCCCT GGCTGCGTTA	360
ATTTGCTTTG TCATTAGGCT TGCGAAGAAC TGCATGTCCT GCGCTACTC TTGTACCAGA	420
TATACTAACT TCCTTCTAGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCCCGTTATC	480
ATAGAGAAAG GGGGTAAGGT TGAGGTCGAA GGTACCTGA TCGACCTCAA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTTTAACC AGAGTTTCAG CGGAACAATG GGGTCGTCCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 26948-2(VA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCCTTTTTT GTGGTGTATC      60
GTGCCGTTCT GTTTGGTGT GCTCGTCAAC GCCAACAGCA GCAGCAGCTC TCATTTTCAG      120
TTGATTATA ACTTGACGCT ATGTGAGCTG AATGGTACAG ATTGGCTGGC AGGAAAATTT      180
GATTGGGCAG TGGAGAGTTT TGTCATTTTT CCCGTGCTGA CCCACATTGT TTCCTATGGT      240
GCACTTACTA CCAGCCATTT CTTGACACA GTCGGTCTGG TTACCGTGTC TACCGCCGGG      300
TTTCTTCACG GGAGGTATGT CCTGAGTAGC ATCTACGCGG TCTGTGCCCT GGCTGCGTTG      360
ATTTGCTTCG TCATTAGGCT TGCGAAGAAC TGCATGTCCT GCGGCTACTC ATGCACCAGA      420
TATACCAACT TCCTTCTAGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCCTGTTATC      480
ATAGAAAAAA AAGGTAAGGT TGAGGTCGAA GGTCACTGA TCGACCTCAA AAGAGTTGTG      540
CTTGATGGTT CCGCGGCAAC TCCTTTAACC AGAGTTTCAC CGGAACAATG GGGTCGTCCC      600
TAG                                                                                   603

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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 41572-2 (NE)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTTCCTT GTGGTGTATC	60
GTGCCGTTCT GGTTCGTGT GCTCGTCAAC GCCAGCAGCA ACAGCAGCTC TCATTTTCAG	120
TTGATTTATA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTGGC TAATAAATTT	180
GATTGGGCAG TGGAGAGTTT TGTCATCTTT CCTGTGTTGA CTCACATTGT TTCCTATGGT	240
GCACTCACTA CTAGCCATTT CCTTGACACA GTCGGTCTGG TTACTGTGTC CACCGCCGGT	300
TTTTTTCACG GCGGGTATGT CTTGAGCAGC ATCTACGCGG TCTGTGCCCT GGCTGCGTTA	360
ATTTGCTTTG TCATTAGGCT TGCGAAGAAC TGCATGTCCT GCGGCTACTC ATGTACCAGA	420
TATACCAACT TCCTTCTGGA CACCAAGGGC AGACTCTATC GTTGGCGGTC GCCCGTTATC	480
ATAGAGAAAA GGGGTAAGGT TGAGGTCGAA GGTCACTGA TCGACCTCAA AAGAGTTGTG	540
CTTGATGGTT CCGCGGCTAC CCCTTTAACC AGAGTTTCAG CGGAACAATG GGGTCGTCCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 42928(IL)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTTCTTT GTGGTGTATC	60
GTGCCGTCCT GGTTCGCTGT GCTCGTCAAC GCCAACAGCG CCAGCAGCTC TCATTGCAG	120
TTGATTTATA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGTTGGC TGACAAGTTT	180
GATTGGGCAG TGGAGACTTT TGTTCTTTAT CCGTGTGTA CTCACATTGT TTCCTATGGT	240
GCACTCACCA CCAGCCATTT CTTGACACA GTCGGTCTGG TTA CTGTGTC CACCGCCGGT	300
TTTGTTACAG GCGGTATGT CTTGAGTAGC ATCTACGCGG TCTGTGCCCT GGCTGCGTTG	360
AGTTGTTTTG TCATCAGGTT TGTGAAGAAC TGCATGTCCT GCGCTACTC ATGTACCAGA	420
TATACCAACT TCCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGATC GCCTGTCATC	480
ATAGAGAAAG GGGGTAAGGT TGAGGTCGAA GGCCATCTGA TCGACCTCAA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTTTAACC AGAGTTTCAG CGGAACGATG GGGTCGTCCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 32983-LG(NC)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGC TGCTCGCGAT TGCTTTCTTT GTGGTGTATC	60
GTGCCGTTCT GTTTGTCTGT GTCGTCAAC GCCAACAGCA GCAGCAGCTC TCATTTTCAG	120
TTGATTTATA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTGGC TGGGGAATTT	180
GATTGGGCGG TGGAAAGTTT TGTCATTTTT CCCGTGTTGA CTCACATTGT TTCCTATGGT	240
GCACTCACTA CTAGCCATTT TCTTGACACA GTCGGTCTGG TTACTGTGTC TACCGCCGGG	300
TTTTTGACG GCGGTATGT CTTGAGCAGC ATCTACGCGG TTTGTGCCCT GGCTGCGTTA	360
ATTTGCTTTG TCATTAGGCT TGCGAAGAAC TGCATGTCCT GGCGCTACTC ATGTACCAGA	420
TATACTAACT TCCTTCTAGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCGCGTTATC	480
ATAGAGAAAG GGGGTAAGGT TGAGGTCGAA GGTCACTCTGA TCGACCTCAA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTTTAACC AGAGTTTCAG CGGAACAATG GGGTCGTCCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 30352-3 (MI)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGTTGGTGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTTTTTT GTGGTGTATC	60
GTGCCGTCCT GTTTGTGTC GCTCGTCAGC GCCAACGCCA ACAGCAGCTC CCATTCACAG	120
TTGATTTACA ACCTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTGTC TAATAAATTT	180
GATTGGGCAG TGGAGTGTTT TGTCATCTTT CCTGTGCTGA CTCACATTGT CTCCTATGGT	240
GCCCTCACTA CCAGCCATTT CCTTGACACA GTCGGTCTGG CCGTTGTGTC TACCGCCGGG	300
TTTGTTCACG GCGGTATGT TCTGAGTAGC ATCTACGCGG TCTGTGCCCT TGCTGCGTTG	360
ATTTGCTTCG TCATTAGATT TGCGAAGAAT TGCATGTCCT GCGGCTACTC ATGTACCAGA	420
TATACCAACT TTCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGGTC ACCTGTCATC	480
ATAGAGAAAA GGGGTAAAGT TGAGGTCGAA GGTAATCTGA TCGACCTCAA GAGAGTTGTG	540
CTTGATGGTT CCGCGGCAAC CCCTATAACC AAAGTTTCAG CGGAACAATG GGGTCATCCT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory
Syndrome Virus
- (B) STRAIN: 47324-2(CAN)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

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ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTTTTTT GTGGTGTATC      60
GTGCCGTCTT GTTTTGTTGT GCTCGTCAAC GCCAACAACA GAAGCAGCTC CCATTTTCAG      120
TTGATTTATA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTGGC TGATAAAATT      180
GATTGGGCAG TGGAGAGTTT TGTCTCTTTT CCCGTTTTGA CTCACATTGT TTCCTATGGT      240
GCCCTAACCA CTAGCCATTT TCTTGACACA GTTGGTCTGG TTACTGTGTC TACCGCTGGT      300
TTTCTTCACG GGCGGTATGT TCTGAGTAGC ATCTACGGCG TCTGCGCCCT GGCTGCGTTG      360
ATTTGCTTTG TCATTAGGTT CGTGAAGAAC TGCATGTCCT GCGCTACTC ATGTACCAGA      420
CATACCAACT TTCTTCTGGA TACCAAGGGC AGACTCTATC GTTGGCGGTC GCCCGTCATC      480
ATAGAGAAAG GGGGTAAAGT TGAGGTCGAA GGTCTCTCA TCGACCTCAA GAGAGTTGTG      540
CTTGATGGTT CCGCGGCAAC CCCTATAACC AGAGTTTCAG CGGAACAATG GGGTCGTCCT      600
TAG                                                                                   603

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(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 18310-A(PA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTTCTTT GTGGTGTATC	60
GTGCCGTTCT GTTTGTCTGT GCTCGTCAAC GCCAACAGCA ACAGCAGCTC TCATTTTCAG	120
TTGATTTATA ACTTGACGCT ATGTGAGCTG AATGGCACAG ACTGGCTGGC TAACAAATTT	180
GATTGGGCAG TGGAGACTTT TGTCATTTTT CCCGTATTGA CTCACATTGT TTCCTATGGT	240
GCACTCACCA CCAGCCATTT CCTTGACACA GTTGGTCTGG TTACTGTGTC CACCGCCGGG	300
TTTTATCAGC GGCGGTATGT CTTGAGTAGC ATCTATGCCG TCTGTGCTCT GGCTGCGTTG	360
TTTTGCTTCG TCATTAGGCT TGCGAAGAAC TGCATGTCCT GGCCTACTC TTGTACCAGA	420
TATACCAACT TCCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCCCGTTATT	480
ATAGAGAAAG GGGGTAAGGT TGAGGTCGAA GGTCACCTGA TCGACCTCAA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTTTAACC AGAGTTTCAG CGGAACAATG GGGTCGTCTC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 24901 (GUA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATGTTGGTGA AATGCTTGAC CGCGGGCCGT TGCTCGCGAT TGCCTTTTTT GTGGTGTATC	60
GTGCCGTTCT GTTTTGCTGT GCTCGTCAAC GCCAACAGCA GCAGCAGCTC TCATTTTCAG	120
TTGATTTATA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTGGC TGACAAATTT	180
GATTGGGCAG TAGAGACTTT TGTCATCTTT CCCGTGTTGA CTCACATTGT TTCCTATGGT	240
GCACTCACCA CCAGCCATTT CCTTGACACA GTTGGTCTGG TTAGTGTC CACCGCCGGG	300
TTTTATCAG GCGGTATGT CTTGAGTAGC ATCTACGCGG TCTGTGCTCT GGCTGCGTTG	360
ATTTGCTTCG TCATTAGGCT TGCGAAGAAC TGCATGTCCT GGCCTACTC TTGTACCAGA	420
TATACCAACT TCCTTCTGGA CACTAAGGGC AGACTCTATC GTTGAGGTC GCCCGTTATC	480
ATACAGAAAG GGGTAAGGT TGAGGTCGAA GGTCACTGA TCGACCTCA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTTTAACC AGAGTTTCAG CGGAACAATG GGGTCGTCCC	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: NADC-8 (IA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGTTGGGGA AATGCTTGAC CGCGGGCTGT TGCTCGCAAT TGCTTTTTTT GTGGTGTATC	60
GTGCCGTCTT GTTTTGTTGC GCTCGTCAGC GCCAACAGCA ACAGCAGCTC AAATTTACAG	120
CTGATTTACA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TAATAAATTT	180
GACTGGGCAG TGGAGTGTTT TGTCACTTTT CCTGTGTTGA CTCACATTGT CTCTTATGGT	240
GCCCTCACTA CTAGCCATTT CCTTGACACA GTCGGTCTGG TCACTGTGTC CACCGCCGGA	300
TTTTTTCACG GGCGGTATGT TCTGAGTAGC ATCTACGCGG TCTGTGCCCT GGCTGCGTTG	360
ATTTGCTTCG TCATTAGGCT TGC GAAGAAT TGCATGTCCT GGC GCTACTC ATGTACCAGA	420
TATACCAACT TTCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCCTGTCATC	480
ATAGAGAAAA GGGGCAAAGT TGAGGTCGAA GGTCACTGA TCGACCTCAA AAGAGTTGTG	540
CTTGATGGTT CCGCGGCAAC CCCTGTAACC AGAGTTTCAG CGGAACAATG GGGTCGTCCT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory
Syndrome Virus
- (B) STRAIN: NADC-9 (IA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATGTTGGTGA AATGCTTGAC CGCGGGCTGT TGCTCGCAAT TGCTTTTTTT GTGGTGTATC	60
GTGTCGTCCT GTTTTGTAGC GCTCGTCAGC GCCAACACGA CCAGCAGCTC AAATTTACAG	120
CTGATTTACA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TAATAAATTT	180
GACTGGGCAG TGGAGTGTTT TGTCATTTTT CCTGTGTTGA CTCACATTGT CTCTTATGGT	240
GCCCTCACTA CTAGCCATTT CCTTGACACA GTCGGTCTGG TCACTGTGTC CACCGCCGGG	300
TTTGTTACAG GGCGGTATGT TCTGAGTAGC ATCTACGCGG TCTGTGCCCT GGCTGCGTTG	360
ATTTGCTTCG TCATTAGGCT TGCGAAGAAC TGCATGTCCT GGCGCTACTC ATGTACCAGA	420
TATACCAACT TTCTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCCTGTCATC	480
GTAGAGAAAA GGGGCAAGGT CGAGGTCGAA GGTCACTGA TCGACCTCAA AAGAGTTGTG	540
CTTGATGGTT CCGCGGCAAC TCCTGTAACC AGAATTTTAT CAGAACAATG GGGTCGTCCT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: RespPRRS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

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ATGTTGGAGA AATGCTTGAC CGCGGGCTGT TGCTCGCAAT TGCTTTCTTT GTGGTGTATC      60
GTGCCGTTCT GTTTTGCTGT GCTCGCCAAC GCCAGCAACG ACAGCAGCTC CCATCTACAG      120
CTGATTTACA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TAACAAATTT      180
GATTGGGCAG TGGAGAGTTT TGTCATCTTT CCCGTTTTGA CTCACATTGT CTCCTATGGT      240
GCCCTCACTA CCAGCCATTT CCTTGACACA GTCGCTTTAG TCACTGTGTC TACCGCCGGG      300
TTTGTTACAG GGCGGTATGT CCTAAGTAGC ATCTACGCGG TCTGTGCCCT GGCTGCGTTG      360
ACTTGCTTCG TCATTAGGTT TGCAAAGAAT TGCATGTCCT GGCGCTACGC GTGTACCAGA      420
TATACCAACT TTCTTCTGGA CACTAAGGGC GGA CTCTATC GTTGGCGGTC GCCTGTCATC      480
ATAGAGAAAA GGGGCAAAGT TGAGGTCGAA GGTCATCTGA TCGACCTCAA AAGAGTTGTG      540
CTTGATGGTT CCGTGGCAAC CCCTATAACC AGAGTTTCAG CGGAACAATG GGGTCGTCCT      600
TAG                                                                    603

```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: 2332 (MN)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATGTTGGAGA AATGCTTGAC CGCGGGCTGT TGCTCGCGAT TGCTTCTTT GTGGTGTATC	60
GTGCCGTTCT GTTTGTCTGT GCTCGCCAAC GCCAGCAACG ACAGCAGCTC CCATCTACAG	120
CTGATTTACA ACTTGACGCT ATGTGAGCTG AATGGCACAG ATTGGCTAGC TAACAAATTT	180
GATTGGGCAG TGGAGAGTTT TGTCACTTTT CCCGTTTGA CTCACATTGT CTCCTATGGT	240
GCCCTCACTA CCAGCCATTT CCTTGACACA GTCGCTTTAG TCACTGTGTC TACCGCCGGG	300
TTTGTTACAG GCGGTATGT CCTAAGTAGC ATCTACGCGG TCTGTGCCCT GGCTGCGTTG	360
ACTTGCTTCG TCATTAGGTT TGCAAAGAAT TGCATGTCCT GCGCTACGC GTGTACCAGA	420
TATACCAACT TTCTTCTGGA CACTAAGGGC AGACTCTATC GTTGGCGGTC GCCTGTCATC	480
ATAGAGAAAA GGGGCAAAGT TGAGGTCGAA GGTCACTCTGA TCGACCTCAA AAGAGTTGTG	540
CTTGATGGTT CCGTGGCAAC CCCTATAACC AGAGTTTCAG CGGAACAATG GGGTCGTCCT	600
TAG	603

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCATTCTGTT GGCAATTGA

20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGCATATATC ATCACTGGCG

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porcine Reproductive and Respiratory Syndrome Virus
- (B) STRAIN: RespPRRS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCATTCTGTT GGCAATTTGA ATGTTTAAGT ATGTTGGAGA AATGCTTGAC CGCGGGCTGT	60
TGCTCGCAAT TGCTTTCTTT GTGGTGTATC GTGCCGTTCT GTTTGTCTGT GCTCGCCAAC	120
GCCAGCAACG ACAGCAGCTC CCATCTACAG CTGATTTACA ACTTGACGCT ATGTGAGCTG	180
AATGGCACAG ATTGGCTAGC TAACAAATTT GATTGGGCAG TGGAGAGTTT TGTCATCTTT	240
CCCGTTTTGA CTCACATTGT CTCCTATGGT GCCCTCACTA CCAGCCATTT CCTTGACACA	300
GTGCGTTTAG TCACTGTGTC TACCGCCGGG TTTGTTACAG GCGGTATGT CCTAAGTAGC	360
ATCTACGCGG TCTGTGCCCT GGCTGCGTTG ACTTGCTTCG TCATTAGGTT TGCAAAGAAT	420
TGCATGTCCT GGCCTACGC GTGTACCAGA TATACCAACT TTCTTCTGGA CACTAAGGGC	480
GGACTCTATC GTTGGCGGTC GCCTGTCATC ATAGAGAAAA GGGGCAAAGT TGAGGTCGAA	540
GGTCATCTGA TCGACCTCAA AAGAGTTGTG CTTGATGGTT CCGTGGCAAC CCCTATAACC	600
AGAGTTTCAG CGGAACAATG GGGTCGTCCT TAGATGACTT CTGTCATGAT AGCACGGCTC	660
CAGAAAAGGT GCTTTTGGCG TTTTCTATTA CCTACACGCC AGTGATGATA TATGCC	716

We Claim:

1. A method for differentiating a first strain of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) from a second strain of said virus comprising the steps:

- a. selecting at least one restriction enzyme which yields a distinctive fragment profile from ORF 5 cDNA from each of said first and second strains;
- b. cleaving the ORF 5 cDNA of said first and second strains with said at least one restriction enzyme;
- c. comparing the restriction enzyme fragment patterns resulting from step (b).

2. The method as described in Claim 1 wherein one of said strains is the vaccine strain RespPRRS® of PRRSV.

3. The method as described in Claim 2 wherein said restriction enzyme is selected from the group consisting of *Mlu* I and *Sfc* I.

4. The method as described in Claim 1 wherein said restriction enzyme is selected from the group consisting of *Mlu* I, *Sfc* I, *Hinc* II and *Sac* II.

5. A kit for differentiating a first strain of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) from a second strain of said virus comprising a pair of primers for amplifying ORF 5 cDNA from each of said first and second strains and at least one restriction enzyme which yields a distinctive fragment profile for the ORF 5 cDNA from each of said first and second strains.

6. The kit of Claim 5 wherein said restriction enzyme is selected from the group consisting of *Mlu* I and *Sfc* I.

7. The kit of Claim 5 wherein said restriction enzyme is selected from the group consisting of *Mlu* I, *Sfc* I, *Hinc* II and *Sac* II.

8. The kit of Claim 5 wherein said primers have the sequence of SEQ ID NO:25 and SEQ ID NO:26.

RespPRRS	ATGTTGGAGA AATGCTTCAC CGCGGGCTGT TGCTCGGAT TGCTTTCTTT	50
VR 2332	ATGTTGGAGA AATGCTTCAC CGCGGGCTGT TGCTCGGAT TGCTTTCTTT	50
Consensus	ATGTTGGAGA AATGCTTCAC CGCGGGCTGT TGCTCGGAT TGCTTTCTTT	50
RespPRRS	GTGGTGTATC GTGCCGTTCT GTTTTGCTGT GCTCGCCAAC GCCAGCAACG	100
VR 2332	GTGGTGTATC GTGCCGTTCT GTTTTGCTGT GCTCGCCAAC GCCAGCAACG	100
Consensus	GTGGTGTATC GTGCCGTTCT GTTTTGCTGT GCTCGCCAAC GCCAGCAACG	100
RespPRRS	ACAGCAGCTC CCATCTACAG CTGATTACA ACTTGACGCT ATGTGAGCTG	150
VR 2332	ACAGCAGCTC CCATCTACAG CTGATTACA ACTTGACGCT ATGTGAGCTG	150
Consensus	ACAGCAGCTC CCATCTACAG CTGATTACA ACTTGACGCT ATGTGAGCTG	150
RespPRRS	AATGGCACAG ATTGGCTAGC TAACAAATTT GATTGGGCAG TGGAGAGTTT	200
VR 2332	AATGGCACAG ATTGGCTAGC TAACAAATTT GATTGGGCAG TGGAGAGTTT	200
Consensus	AATGGCACAG ATTGGCTAGC TAACAAATTT GATTGGGCAG TGGAGAGTTT	200
RespPRRS	TGTCATCTTT CCCGTTTGA CTCACATTGT CTCTATGGT GCCCTCACTA	250
VR 2332	TGTCATCTTT CCCGTTTGA CTCACATTGT CTCTATGGT GCCCTCACTA	250
Consensus	TGTCATCTTT CCCGTTTGA CTCACATTGT CTCTATGGT GCCCTCACTA	250
RespPRRS	CCAGCCATTT CCTTGACACA GTCCGTTTAG TCACTGTGTC TACCGCCGGG	300
VR 2332	CCAGCCATTT CCTTGACACA GTCCGTTTAG TCACTGTGTC TACCGCCGGG	300
Consensus	CCAGCCATTT CCTTGACACA GTCCGTTTAG TCACTGTGTC TACCGCCGGG	300
RespPRRS	TTTGTTACG GCGGATATGT CCTAAGTAGC ATCTACGCGG TCTGTGCCCT	350
VR 2332	TTTGTTACG GCGGATATGT CCTAAGTAGC ATCTACGCGG TCTGTGCCCT	350
Consensus	TTTGTTACG GCGGATATGT CCTAAGTAGC ATCTACGCGG TCTGTGCCCT	350
RespPRRS	GGCTGCGTTG ACTTGCTTCG TCATTAGGTT TGCAAAGAAT TGCATGTCCT	400
VR 2332	GGCTGCGTTG ACTTGCTTCG TCATTAGGTT TGCAAAGAAT TGCATGTCCT	400
Consensus	GGCTGCGTTG ACTTGCTTCG TCATTAGGTT TGCAAAGAAT TGCATGTCCT	400
RespPRRS	GGCGCTACGC GTGTACCAGA TATACCAACT TTCTTCTGGA CACTAAGGGG	450
VR 2332	GGCGCTACGC GTGTACCAGA TATACCAACT TTCTTCTGGA CACTAAGGGG	450
Consensus	GGCGCTACGC GTGTACCAGA TATACCAACT TTCTTCTGGA CACTAAGGGG	450
RespPRRS	CGACTCTATC GTTGCGGTC GCCTGTCATC ATAGAGAAAA GGGGCAAAGT	500
VR 2332	CGACTCTATC GTTGCGGTC GCCTGTCATC ATAGAGAAAA GGGGCAAAGT	500
Consensus	CGACTCTATC GTTGCGGTC GCCTGTCATC ATAGAGAAAA GGGGCAAAGT	500
RespPRRS	TGAGGTCGAA GGTCACTCTGA TCGACCTCAA AAGAGTTGTG CTTGATGGTT	550
VR 2332	TGAGGTCGAA GGTCACTCTGA TCGACCTCAA AAGAGTTGTG CTTGATGGTT	550
Consensus	TGAGGTCGAA GGTCACTCTGA TCGACCTCAA AAGAGTTGTG CTTGATGGTT	550
RespPRRS	CCGTGGCAAC CCTATAACC AGAGTTTCAG CGGAACAATG GGGTCGTCCT	600
VR 2332	CCGTGGCAAC CCTATAACC AGAGTTTCAG CGGAACAATG GGGTCGTCCT	600
Consensus	CCGTGGCAAC CCTATAACC AGAGTTTCAG CGGAACAATG GGGTCGTCCT	600
RespPRRS	TAG	603
VR 2332	TAG	603
Consensus	TAG	603

FIG. 1

RespPRRS	ATGTTGGACA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
VR 2332	ATGTTGGACA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
#1	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
#2	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
#3	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
#4	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
#5	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
#6	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
#7	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
#8	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
#9	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
#10	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
#11	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
#12	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
#13	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
#14	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
#15	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
#16	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
#17	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
#18	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
#19	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
#20	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
NADC-8	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
NADC-9	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50
Consensus	ATGTTGGCA	PATGCTTGAC	CGCGGCTGT	TGCTGGCAT	TGCTTTTIT	50

RespPRRS	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
VR 2332	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
#1	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
#2	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
#3	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
#4	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
#5	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
#6	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
#7	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
#8	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
#9	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
#10	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
#11	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
#12	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
#13	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
#14	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
#15	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
#16	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
#17	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
#18	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
#19	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
#20	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
NADC-8	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
NADC-9	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100
Consensus	GTGGTATATC	GTGCGGTTC	GTATTGCTGT	GCTCGGAC	GCCAGACAGG	100

FIG. 2A

RespPRRS	ACAGCAGCTC	CCATCTACAG	CTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
VR 2332	ACAGCAGCTC	CCATCTACAG	CTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
#1	ACAGCAGCTC	AAATTTACAG	CTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
#2	ACAGCAGCTC	CCATTTACAG	CTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
#3	ACAGCAGCTC	TCATTTACAG	CTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
#4	ACAGCAGCTC	TCATCTCAA	TTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
#5	ACAGCAGCTC	AAATTTACAG	CTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
#6	CCAGCAGCTC	CCATTTACAG	TTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
#7	ACAGCAGCTC	TCATTTACAG	TTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
#8	CCAGCAGCTC	TCATTCACAG	TTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
#9	ACAGCAGCTC	TCATCTCAA	TTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
#10	CCAGCAGCTC	TCATTTACAG	TTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
#11	ACAGCAGCTC	TCATTCACAG	TTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
#12	CCAGCAGCTC	TCATTTACAG	TTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
#13	CCAGCAGCTC	TCATTTACAG	TTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
#14	ACAGCAGCTC	TCATTTACAG	TTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
#15	CCAGCAGCTC	TCATTTACAG	TTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
#16	CCAGCAGCTC	TCATTTACAG	TTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
#17	ACAGCAGCTC	TCATTCACAG	TTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
#18	GAAGCAGCTC	CCATTTACAG	TTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
#19	ACAGCAGCTC	TCATTTACAG	TTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
#20	CCAGCAGCTC	TCATTTACAG	TTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
NADC-8	ACAGCAGCTC	AAATTTACAG	CTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
NADC-9	CCAGCAGCTC	AAATTTACAG	CTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150
Consensus	VMAGCAGCTC	MAATTTACAG	TTGATTTACA	ACGTGACGCT	ATGTGAGCTG	150

RespPRRS	AATGGACAG	AATGGATAC	TAACAAATTT	GATGGGGCG	TGAGAGCTT	200
VR 2332	AATGGACAG	AATGGATAC	TAACAAATTT	GATGGGGCG	TGAGAGCTT	200
#1	AATGGACAG	AATGGATAC	TAATAAATTT	GATGGGGCG	TGAGAGCTT	200
#2	AATGGACAG	AATGGATAC	TAGTAGATTT	GATGGGGCG	TGAGAGCTT	200
#3	AATGGACAG	AATGGATAC	TAATAAATTT	GATGGGGCG	TGAGAGCTT	200
#4	AATGGACAG	AATGGATAC	TGATAGATTT	GATGGGGCG	TGAGAGCTT	200
#5	AATGGACAG	AATGGATAC	TAATAAATTT	GATGGGGCG	TGAGAGCTT	200
#6	AATGGACAG	AATGGATAC	TAATAAATTT	GATGGGGCG	TGAGAGCTT	200
#7	AATGGACAG	AATGGATAC	TAACAAATTT	GATGGGGCG	TGAGAGCTT	200
#8	AATGGACAG	AATGGATAC	TAGTAAATTT	GATGGGGCG	TGAGAGCTT	200
#9	AATGGACAG	AATGGATAC	TGATAGATTT	GATGGGGCG	TGAGAGCTT	200
#10	AATGGACAG	AATGGATAC	TAACAAATTT	GATGGGGCG	TGAGAGCTT	200
#11	AATGGACAG	AATGGATAC	TAATAAATTT	GATGGGGCG	TGAGAGCTT	200
#12	AATGGACAG	AATGGATAC	TGAGAAATTT	GATGGGGCG	TGAGAGCTT	200
#13	AATGGACAG	AATGGATAC	AGGAAATTT	GATGGGGCG	TGAGAGCTT	200
#14	AATGGACAG	AATGGATAC	TAATAAATTT	GATGGGGCG	TGAGAGCTT	200
#15	AATGGACAG	AATGGATAC	TGACAAATTT	GATGGGGCG	TGAGAGCTT	200
#16	AATGGACAG	AATGGATAC	TGGGAAATTT	GATGGGGCG	TGAGAGCTT	200
#17	AATGGACAG	AATGGATAC	TAATAAATTT	GATGGGGCG	TGAGAGCTT	200
#18	AATGGACAG	AATGGATAC	TGATAAATTT	GATGGGGCG	TGAGAGCTT	200
#19	AATGGACAG	AATGGATAC	TAACAAATTT	GATGGGGCG	TGAGAGCTT	200
#20	AATGGACAG	AATGGATAC	TGACAAATTT	GATGGGGCG	TGAGAGCTT	200
NADC-8	AATGGACAG	AATGGATAC	TAATAAATTT	GATGGGGCG	TGAGAGCTT	200
NADC-9	AATGGACAG	AATGGATAC	TAATAAATTT	GATGGGGCG	TGAGAGCTT	200
Consensus	AATGGACAG	AATGGATAC	WRRNRRRTT	GATGGGGCG	TGAGAGCTT	200

FIG. 2B

RespRRS	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
VR 2332	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
#1	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
#2	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
#3	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
#4	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
#5	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
#6	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
#7	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
#8	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
#9	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
#10	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
#11	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
#12	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
#13	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
#14	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
#15	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
#16	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
#17	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
#18	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
#19	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
#20	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
NADC-8	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
NADC-9	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250
Consensus	TGTCATGTTT	CCCGTGTGA	CCACATTGT	TTCTATGCT	GCCTGACAA	250

RespRRS	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
VR 2332	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
#1	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
#2	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
#3	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
#4	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
#5	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
#6	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
#7	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
#8	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
#9	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
#10	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
#11	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
#12	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
#13	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
#14	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
#15	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
#16	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
#17	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
#18	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
#19	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
#20	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
NADC-8	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
NADC-9	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300
Consensus	CCAGCCATTT	CTTGACACA	TTGGTTTGG	TCACGTGTGC	TACCGCGGG	300

FIG. 2C

RespPRRS	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
VR 2332	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
#1	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
#2	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
#3	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
#4	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
#5	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
#6	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
#7	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
#8	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
#9	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
#10	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
#11	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
#12	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
#13	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
#14	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
#15	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
#16	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
#17	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
#18	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
#19	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
#20	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
NADC-8	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
NADC-9	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350
Consensus	TTTCTTCC	GGCGGTATGT	CTTACAGTAC	ATCTAGCCG	TGTGGGCT	350

RespPRRS	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
VR 2332	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
#1	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
#2	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
#3	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
#4	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
#5	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
#6	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
#7	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
#8	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
#9	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
#10	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
#11	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
#12	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
#13	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
#14	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
#15	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
#16	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
#17	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
#18	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
#19	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
#20	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
NADC-8	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
NADC-9	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400
Consensus	GGCGCGTTG	ACTTGGTTG	TCATAGGTT	AGCGAAGAA	TGCATGTC	400

FIG. 2D

RespPRRS	GGCGCTATCC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
VR 2332	GGCGCTATCC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
#1	GGCGCTATTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
#2	GGCGCTATTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
#3	GGCGCTATTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
#4	GGCGCTACTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
#5	GGCGCTACTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
#6	GGCGCTACTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
#7	GGCGCTACTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
#8	GGCGCTACTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
#9	GGCGCTACTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
#10	GGCGCTACTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
#11	GGCGCTACTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
#12	GGCGCTACTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
#13	GGCGCTACTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
#14	GGCGCTACTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
#15	GGCGCTACTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
#16	GGCGCTACTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
#17	GGCGCTACTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
#18	GGCGCTACTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
#19	GGCGCTACTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
#20	GGCGCTACTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
NADC-8	GGCGCTACTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
NADC-9	GGCGCTACTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450
Consensus	GGCGCTATTC	HTGTACGAGA	TATACCAACT	TCTTCTCTGA	CACAAAGGGC	450

RespPRRS	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAA	GCGGTAAGGT	500
VR 2332	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAA	GCGGTAAGGT	500
#1	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500
#2	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAA	GCGGTAAGGT	500
#3	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500
#4	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500
#5	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500
#6	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500
#7	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500
#8	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500
#9	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500
#10	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500
#11	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500
#12	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500
#13	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500
#14	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500
#15	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500
#16	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500
#17	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500
#18	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500
#19	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500
#20	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500
NADC-8	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500
NADC-9	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500
Consensus	AGACTCTATC	GTTGGCGGTC	CCCGCTATC	ATAGACAAAG	GCGGTAAGGT	500

FIG. 2E

RespRRS	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
VR 2332	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
#1	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
#2	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
#3	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
#4	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
#5	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
#6	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
#7	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
#8	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
#9	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
#10	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
#11	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
#12	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
#13	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
#14	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
#15	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
#16	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
#17	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
#18	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
#19	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
#20	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
NADC-8	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
NADC-9	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550
Consensus	TCAGGTCGAA	GCTCACTTCA	TTCAGCTCPA	PAGAGTTGTG	CTTGATGGTT	550

RespRRS	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
VR 2332	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
#1	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
#2	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
#3	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
#4	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
#5	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
#6	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
#7	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
#8	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
#9	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
#10	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
#11	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
#12	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
#13	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
#14	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
#15	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
#16	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
#17	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
#18	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
#19	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
#20	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
NADC-8	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
NADC-9	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600
Consensus	CCGCGGCGAC	CCCTTTAACC	AGAATTTTCAG	CGGAACHATG	GGGTCTTCCT	600

FIG. 2F

RespPRRS	TAG	603
VR 2332	TAG	603
#1	TAG	603
#2	TAG	603
#3	TAG	603
#4	TAG	603
#5	TAG	603
#6	TAG	603
#7	TAG	603
#8	TAG	603
#9	TAG	603
#10	TAG	603
#11	TAG	603
#12	TAG	603
#13	TAG	603
#14	TAG	603
#15	TAG	603
#16	TAG	603
#17	TAG	603
#18	TAG	603
#19	TAG	603
#20	TAG	603
NADC-8	TAG	603
NADC-9	TAG	603
Consensus	TAG	603

FIG. 2G

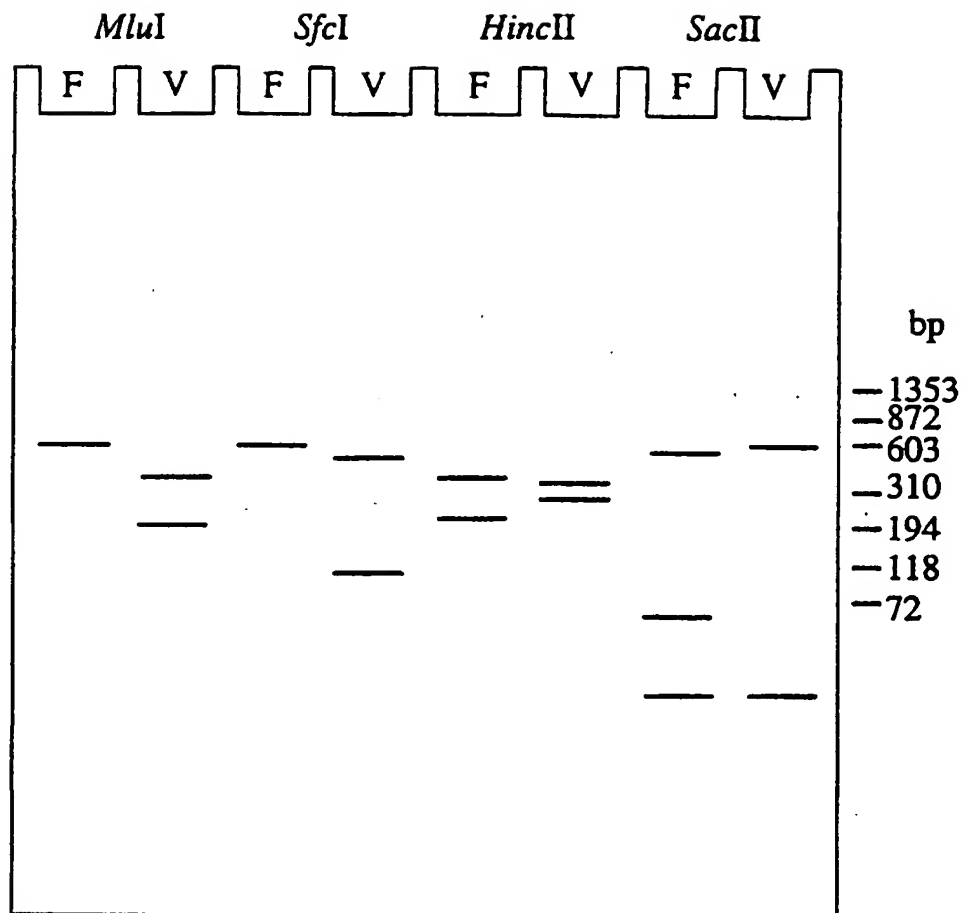


FIG. 3

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US97/03126

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : Please See Extra Sheet.

US CL : 435/106, 108, 109, 110, 115, 235.1, 239; 424/204.1, 218.1, 815

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/106, 108, 109, 110, 115, 235.1, 239; 424/204.1, 218.1, 815

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, MEDLINE, CAPLUS, CABA, WPIDS

SEARCH TERMS: LELYSTAD, PRRSV, PEARS, MSD, RESTRICTION ENZYME, CLONE, SEQUENCE, DETECTION, SSLP

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	MENG et al. Molecular cloning and nucleotide sequencing of the 3'-terminal genomic RNA of the porcine reproductive and respiratory syndrome virus. Journal of General Virology. 1994. Vol. 75. pages 1795-1801, see entire document.	1-8
Y	KAPUR et al. Genetic variation in porcine reproductive and respiratory syndrome virus isolates in the midwestern United States. Journal of General Virology. 1996. Vol. 77. pages 1271-1276, see entire document.	1-8



Further documents are listed in the continuation of Box C.



See patent family annex.

*

Special categories of cited documents:

T

later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

A

document defining the general state of the art which is not considered to be of particular relevance

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document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

E

earlier document published on or after the international filing date

Y

document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

L

document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reasons (as specified)

O

document referring to an oral disclosure, use, exhibition or other means

A

document member of the same patent family

P

document published prior to the international filing date but later than the priority date claimed

Date of the actual completion of the international search

04 JUNE 1997

Date of mailing of the international search report

06.08.97

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US97/03126

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	MENG et al. Sequence comparison of open reading frames 2 to 5 of low and high virulence United States isolates of porcine reproductive and respiratory syndrome virus. Journal of General Virology. 1995. Vol. 76. pages 3181-3188, see entire document.	1-8
Y	SUAREZ et al. Direct detection of the porcine reproductive and respiratory syndrome (PRRS) virus by reverse polymerase chain reaction (RT-PCR). Arch. Virol., 1994. Vol. 135. pages 89-99, see entire document.	1-8
Y	WO 92/21375 (STICHTING CENTRAAL DIERGENEESKUNDIG INSTITUUT) 10 December 1992 (10-12-92), see entire document.	1-8 -
Y	VILGALYS et al. Rapid Genetic Identification and Mapping of Enzymatically Amplified Ribosomal DNA from Several Cryptococcus Species. Journal of Bacteriology. August 1990. Vol. 172, No. 8. pages 4238-4246, see entire document.	1-8
Y	JAYARAO et al. Differentiation of Streptococcus uberis from Streptococcus parauberis by Polymerase Chain Reaction and Restriction Fragment Length Polymorphism Analysis of 16S Ribosomal DNA. Journal of Clinical Microbiology. December 1991. Vol. 29, No. 12. pages 2774-2778, see entire document.	1-8
Y	MARCONI et al. Phylogenetic Analysis of the Genus Borrelia : a Comparison of North american and European Isolates of Borrelia burgdorferi. Journal of Bacteriology. January 1992. Vol. 174, No. 1. pages 241-244, see entire document.	1-8
A	SAITO et al. Characteristics of Major Structural Protein Coding Gene and Leader-Body Sequence in Subgenomic mRNA of Porcine Reproductive and Respiratory Syndrome Virus Isolated in Japan. Journal Vet. Med. Sci. 1996. Vol. 58, No. 4. pages 377-380, see entire document.	1-8
A	MENG et al. Development of a radiolabeled nucleic acid probe for the detection of encephalomyocarditis virus of swine. J. Vet. Diagn. Invest. 1993. Vol. 5. pages 254-258, see entire document.	1-8
A	MARDASSI et al. Identification of major differences in the nucleocapsid protein genes of a Quebec strain and European strains of porcine reproductive and respiratory syndrome virus. Journal of General Virology. March 1994. Vol. 75. pages 681-685, see entire document.	1-8

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/03126

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	MENG et al. Phylogenetic analyses of the putative M (ORF 6) and N (ORF 7) genes of porcine reproductive and respiratory syndrome virus (PRRSV): implication for the existence of two genotypes of PRRSV in the U.S.A. and Europe. Arch. Virology. 1995, Vol. 140, pages 745-755, see entire document.	1-8

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US97/03126

A. CLASSIFICATION OF SUBJECT MATTER:

IPC (6):

A61K 39/12; C12N 7/00, 7/02; C12P 13/04, 13/24, 13/22, 13/20, 13/14, 13/08